

RL J. BIOL. CHEM. 267:21172-21178(1992). HIGH AFFINITY FOR TNA-ALPHA AND
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-BETA.
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
 CC -1- PAM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
 CC LEVEL ON THREONINE RESIDUES.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC EMBL: M3315; G189186; -
 DR EMBL: M35857; G339752; -
 DR EMBL: M35994; G339758; -
 DR PIR: A35356; A35356.
 DR PIR: A36007; A36007.
 DR PIR: A36475; A36475.
 DR PIR: B35010; B35010.
 DR PIR: A23666; A23666.
 DR HSP: P19438; 1TNR.
 DR MIM: 19191; -
 DR PROSITE: PS00652; TNFR_NGFR.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL;
 KW PHOSPHORYLATION.
 FT SIGNAL 1 22 TUMOR NECROSIS FACTOR RECEPTOR 2.
 FT CHAIN 23 461 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 258 287 POTENTIAL.
 FT TRANSMEM 288 461 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 288 461 4 X TNFR-CYS.
 FT DOMAIN 39 201 TNFR-CYS 1.
 FT REPEAT 39 76 TNFR-CYS 2.
 FT REPEAT 77 118 TNFR-CYS 3.
 FT REPEAT 119 162 TNFR-CYS 4.
 FT REPEAT 163 201 TNFR-CYS 1.
 FT REPEAT 163 201 BY SIMILARITY.
 FT DISULFID 40 53 BY SIMILARITY.
 FT DISULFID 54 67 BY SIMILARITY.
 FT DISULFID 57 75 BY SIMILARITY.
 FT DISULFID 78 93 BY SIMILARITY.
 FT DISULFID 96 110 BY SIMILARITY.
 FT DISULFID 100 118 BY SIMILARITY.
 FT DISULFID 120 126 BY SIMILARITY.
 FT DISULFID 134 143 BY SIMILARITY.
 FT DISULFID 137 161 BY SIMILARITY.
 FT DISULFID 164 179 BY SIMILARITY.
 FT CARBOHYD 171 171 POTENTIAL.
 FT CARBOHYD 193 193 R -> P (IN REF. 3).
 FT CONFLICT 141 141 R -> M (IN REF. 1).
 FT CONFLICT 196 196 R -> T (IN REF. 3).
 FT CONFLICT 363 363 A -> T (IN REF. 3).
 FT SEQUENCE 461 AA; 48316 MW; 0F5D0C44 CRC32;
 SQ SEQUENCE 461 AA; 48316 MW; 0F5D0C44 CRC32;
 Query Match 14.2%; Score 405; DB 9; Length 461;
 Best Local Similarity 41.8%; Pred. No. 6,30e-63;
 Matches 69; Conservative 26; Mismatches 59; Indels 11; Gaps 8;

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN SEQUENCE FROM N.A.
 RP MEDLINE; 9118785.
 RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
 RA WONG G.H., CHEN E.Y., GOEDEL D.V.,
 RA PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91246168.
 RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
 RA COPELAND N.G., JENKINS N.A., SMITH C.A.,
 RL MOL. CELL. BIOL. 11:3020-3026(1991).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC EMBL: M60469; G199828; -
 DR EMBL: M59378; G202095; -
 DR PIR: B3634; B3634.
 DR HSP: P19438; 1TNR.
 DR PROSITE: PS00652; TNFR_NGFR.
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
 KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 22 TUMOR NECROSIS FACTOR RECEPTOR 2.
 FT CHAIN 23 474 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 258 288 POTENTIAL.
 FT TRANSMEM 288 474 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 288 474 4 X TNFR-CYS.
 FT DOMAIN 39 203 TNFR-CYS 1.
 FT REPEAT 39 77 TNFR-CYS 2.
 FT REPEAT 78 119 TNFR-CYS 3.
 FT REPEAT 120 164 TNFR-CYS 4.
 FT REPEAT 165 203 TNFR-CYS 1.
 FT REPEAT 165 203 BY SIMILARITY.
 FT DISULFID 40 54 BY SIMILARITY.
 FT DISULFID 55 68 BY SIMILARITY.
 FT DISULFID 58 76 BY SIMILARITY.
 FT DISULFID 79 94 BY SIMILARITY.
 FT DISULFID 97 111 BY SIMILARITY.
 FT DISULFID 101 127 BY SIMILARITY.
 FT DISULFID 121 145 BY SIMILARITY.
 FT DISULFID 139 163 BY SIMILARITY.
 FT DISULFID 166 181 BY SIMILARITY.
 FT CARBOHYD 69 69 POTENTIAL.
 FT CARBOHYD 195 195 POTENTIAL.
 FT SEQUENCE 474 AA; 50319 MW; DC32B286 CRC32;
 SQ SEQUENCE 474 AA; 50319 MW; DC32B286 CRC32;
 Query Match 13.1%; Score 375; DB 9; Length 474;
 Best Local Similarity 41.5%; Pred. No. 3.56e-56;
 Matches 66; Conservative 21; Mismatches 61; Indels 11; Gaps 7;

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUThERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 89356608.
 RX STAMENKOVIC I., CLARK E.A., SEED B.;
 RL EMO J. 8:1403-1410(1989).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; X60592; G29851; -
 DR PIR; S04460; S04460.
 DR MIR; 109335; -
 DR PROSITE; PS00652; TNFR_NGFR.
 KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 277
 FT DOMAIN 20 193
 FT TRANSMEM 194 215
 FT DOMAIN 216 277
 FT DOMAIN 25 187
 FT REPEAT 25 187
 FT REPEAT 61 103
 FT REPEAT 104 144
 FT REPEAT 145 187
 FT CARBOHYD 153 153
 FT CARBOHYD 180 180
 SQ SEQUENCE 277 AA; 30619 MW; 3B284411 CRC32;

Query Match 10.6%; Score 303; DB 2; Length 277;
 Best Local Similarity 36.8%; Pred. No. 2,64e-40;
 Matches 56; Conservative 21; Mismatches 67; Indels 8; Gaps 7;

Db 38 csclqpgqklysdctefetecldpcgesefldvnmrethchqklycdpn-lylr-vyqkg 95
 41 CDKCPPTLYLKQHTAKMTKATVCAPDPHYTDSWHTSDEC-L--YCSVCKELQYVQEC 97
 QY 96 tsetdtctceegwhctseacscvllhscspgfgvqkqatvgsdltcepcvpgffnvs 155
 98 NRTNHRVCECKEGRY-L-EI-EFCLKHSRCPGFGVQAGTPERNVTCRCRCPDGFSSNET 154
 Db 156 safekchpwtscetkdlvvgagqntcdvvcg 187
 155 SSKAPCRKHTNCVFGLLTQKGNATHDNICS 186
 QY

RESULT 4
 ID VT2.MYXVL STANDARD; PRT; 289 AA.
 AC P27512;
 DT 01-APR-1992 (REL. 23, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40).
 GN CDM40.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUThERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 92105763.
 RX TORRES R.M., CLARK E.A.;
 RL J. IMMUNOL. 148:620-626(1992).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 ANTI-VIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; M95181; G332310; -
 DR EMBL; A23729; E199442; -
 DR PIR; A40566; G0VZML.
 DR HSSP; P19438; ITNR.
 DR PROSITE; PS00652; TNFR_NGFR.
 KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 16
 FT CHAIN 17 326
 FT DOMAIN 27 186

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUThERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 92105763.
 RX TORRES R.M., CLARK E.A.;
 RL J. IMMUNOL. 148:620-626(1992).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 ANTI-VIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; M95181; G332310; -
 DR EMBL; A23729; E199442; -
 DR PIR; A40566; G0VZML.
 DR HSSP; P19438; ITNR.
 DR PROSITE; PS00652; TNFR_NGFR.
 KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 16
 FT CHAIN 17 326
 FT DOMAIN 27 186

RA HOWARD M., COCKRAYNE D.A.;
 RL J. IMMUNOL. 149:3921-3926(1992).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; M83312; G1553059; -
 DR EMBL; M94126; G192526; -
 DR EMBL; M94128; G192526; JOINED.
 DR EMBL; M94127; G192526; JOINED.
 DR PIR; A46476; A46476.
 DR HSSP; P19438; ITNR.
 DR PROSITE; PS00652; TNFR_NGFR.
 KW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 289
 FT DOMAIN 20 193
 FT TRANSMEM 194 215
 FT DOMAIN 216 289
 FT DOMAIN 25 187
 FT REPEAT 25 187
 FT REPEAT 61 103
 FT REPEAT 104 144
 FT REPEAT 145 187
 FT CARBOHYD 153 153
 SQ SEQUENCE 289 AA; 32111 MW; D8D70A2C CRC32;

Query Match 10.3%; Score 294; DB 2; Length 289;
 Best Local Similarity 38.8%; Pred. No. 2,31e-38;
 Matches 59; Conservative 20; Mismatches 65; Indels 8; Gaps 6;

Db 38 cdicpgsrlsthtactekqchpcdsgefsaqwnreirchqhncpn-qgllr-vkkg 95
 41 CDKCPPTLYLKQHTAKMTKATVCAPDPHYTDSWHTSDEC-LX--CSVCKELQYVQEC 97
 QY 96 taedtyctckegqchskcscacaghtpctprfgymettdtctchpcvpgffnvs 155
 98 NRTNHRVCECKEGRY-L-EI-EFCLKHSRCPGFGVQAGTPERNVTCRCRCPDGFSSNET 154
 Db 156 sflekcyptscedknleivlqgtsqtnvvcg 187
 155 SSKAPCRKHTNCVFGLLTQKGNATHDNICS 186
 QY

RESULT 5
 ID VT2.MYXVL STANDARD; PRT; 326 AA.
 AC P29825;
 DT 01-APR-1993 (REL. 25, CREATED)
 DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
 DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
 GN T2.
 OS MYXOMA VIRUS (STRAIN LAUSANNE).
 OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXYVIRIDAE; CHOROPOXVIRINAE;
 OC LEPOPOVIRUSES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 9135768.
 RX UPTON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;
 RL VIROLOGY 184:370-382(1991).
 CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
 ANTI-VIRAL EFFECTS OF THE CYTOKINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; M95181; G332310; -
 DR EMBL; A23729; E199442; -
 DR PIR; A40566; G0VZML.
 DR HSSP; P19438; ITNR.
 DR PROSITE; PS00652; TNFR_NGFR.
 KW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
 FT SIGNAL 1 16
 FT CHAIN 17 326
 FT DOMAIN 27 186

Query Match	Similarity	Score	DB %	Length
Best Local	28.9%	Pred. No. 3,53e-32;		
Matches 54;	Conservative	30; Mismatches 92; Indels 11; Gaps 8;		
Db	52	emphdvccsrppgefvfvcvsgdvctcktpbnsynehnhlstdcqlnfp-cdiylgfl	110	
Qy	34	ETSHQLDCKCPGHYYLKHQHTAKWKTYCACCPHHYTDWHTSDECLYSPVKE-LQY	92	
Db	111	eevaptcdtkraecrcqpgmascvyladnecvnceeerlylcpgteaevtelmdtdncv	170	
Qy	93	VK-QECNRTNHNVCCKRGR---YIEIF-FCLKHR-S-CPPGFGV-VQAGTPERNVCK	143	
Db	171	pekpghfngtsspraircqphtceiqglveaapgtysedtlcknppepmanllajlsl	230	
Qy	144	RCPDGFEFSMETSKAPCRKHTCSVFGLLTOKGNATHDNCISGNSSTOKCGIDVITCE	203	
Db	231	viflilt 237		
Qy	204	EAFERFA 210		
RESULT	7	STANDARD;	PRT;	325 AA.
ID	VT2 SEVKA			
AC	P25943;			
DT	01-MAY-1992 (REL. 22, CREATED)			
DT	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)			
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DE	TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).			
GN	T2.			
OS	SHOPE FIBROBLAST VIRUS (STRAIN KASZA) (SEV)			
OC	VARIDAE; DS-DNA ENVELOPED VIRUSES; POXVIRIDAE; CHORDOPOXVIRINAE;			
OC	LEPORIPOXVIRUSES.			
RN	[1]			
RX	SEQUENCE FROM N.A.			
RX	MEDLINE; 87321103.			
RA	UPTON C., DELANGE A.M., MCPADDEN G.;			
RA	VIROLOGY 160:20-30(1987).			
CC	[2]			
CC	FUNCTION.			
CC	MEDLINE; 91207415.			
CC	SMITH C.A., DAVIS T., WIGNALL J.M., DIN W.S., FARRAH T., UPTON C.,			
CC	MCPADDEN G., GOODMAN R.G.;			
CC	BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).			
CC	-I- FUNCTION: BINDS TO TNF-ALPHA AND BETA, PROBABLY PREVENTS TNF TO			
CC	REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL			
CC	ANTIVIRAL EFFECTS OF THE CYTOKINE.			
CC	-I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	EMBL; M17433; -; NOT ANNOTATED_CDS.			
DR	EMBL; A23727; E199408; -			
DR	PIR; B43692;			
DR	HSSP; P19438; 11NR.			
DR	PROSITE; PS00652; TNFR_NGFR.			
KW	RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.			
FT	SIGNAL	1	16	POTENTIAL.
FT	CHAIN	17	325	PROTEIN T2.
FT	DOMAIN	27	186	4 X TNFR-CYS.
FT	REPEAT	27	62	TNFR-CYS 1.
FT	REPEAT	63	104	TNFR-CYS 2.
FT	REPEAT	105	147	TNFR-CYS 3.
FT	REPEAT	148	186	TNFR-CYS 4.
FT	CARBOHYD	105		POTENTIAL.
FT	CARBOHYD	181		POTENTIAL.
FT	CARBOHYD	205		POTENTIAL.
FT	CARBOHYD	238		POTENTIAL.

[illegible]

FT	CARBONYD	177	177	POTENTIAL.
SO	SEQUENCE	435 AA;	46709 MW;	203882DD CRC32;
	Query Match	9.1%;	Score 260;	DB 9; Length 435;
	Best Local Similarity	32.3%;	Pred. No. 3,98e-31;	
	Matches	52;	Conservative	23; Mismatches 75; Indels 11; Gaps 6;
Db	52	epghrlccscppgttyvsakcsrlrdtvcacscensynehmnylltclqlrcdpdv-mgl 110		
OY	34	ETSHQLDCKCPPTIYLKQHCTAKMTVCAPCPDHYTDSMHTSDEC-LY--CSYCKEL 90		
Db	111	eeiap-ctskrtktcrgpnmfcaaalecthecllsdcpptgeaelkdevgkgnhcy 169		
OY	91	QYVQECMRTNRRVCECKEGRY-----LEIEFCLKHRSCEPFGV-VQAGTPERNTVCKR 144		
Db	170	ckaghfgntssparcqbphtrcengcgviveapnqasdttc 210		
OY	145	CPDGFSSNETSKAPCKRKHNTCSVFGILLIKGNATINDNIC 185		
RESULT	9	STANDARD;	PRT;	349 AA.
ID	VC22 VAR			
AC	P34015;			
DT	01-FEB-1994 (REL. 28, CREATED)			
DT	01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)			
DE	01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)			
DT	PROTEIN C22/B28 HOMOLOG.			
GN	GAR.			
OS	VARIOLA VIRUS.			
OC	VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXYVIRIDAE; CHORDOPXYVIRINAE;			
OC	ORTHOPOXVIRUSES.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-INDIA-1967 / ISOLATE IND3;			
RL	MEDLINE: 93202281.			
RA	SHCHELKUNOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.;			
CC	FEB5 LETT. 319:80-83(1993).			
-I	-I SIMILARITY: CONTAINS TWO LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.			
DR	EMBL: X69198; G457087. -			
DR	EMBL: X67117; G516449; -			
DR	PIR: D36858; D36858.			
DR	PIR: S35987; S35987.			
DR	PIR: S46888; S46888.			
DR	HSSP: P19438; 1TNR.			
DR	PROSITE: PS00652; TNFR_NGFR.			
KW	REPEAT.			
FT	DOMAIN	31	108	2 X TNFR-CYS.
FT	REPEAT	31	66	TNFR-CYS 1.
FT	REPEAT	67	108	TNFR-CYS 2.
SO	SEQUENCE	349 AA;	38189 MW;	50DDB435 CRC32;
	Query Match	8.0%;	Score 230;	DB 10; Length 349;
	Best Local Similarity	35.4%;	Pred. No. 6.55e-25;	
	Matches	46;	Conservative	19; Mismatches 58; Indels 7; Gaps 4;
Db	40	hnlclscppatyasrlcdskntcpcgsgttsrnhlpaciscngscnsgvqetrs 99		
OY	37	HQLDCKCPPTIYLKQHCTAKMTVCAPCPDHYTDSMHTSDECLYCSYCKELQYVKOE 96		
Db	100	enthnrlccscppgyllkxsgsgkacvsgtkcglsygyvs-ghtsvgdvlscpccfgty 158		
OY	97	CNRTHNRCVCECKEGRY--LE--IE--FCLHRSCEPFGVVGAGTPERNTVCKRCRPGDF 150		
Db	159	shvtsadck 168		
OY	151	SNETSKAPC 160		
RESULT	10	STANDARD;	PRT;	454 AA.
ID	TNRL MOUSE			
AC	P25118;			
DT	01-MAY-1992 (REL. 22, CREATED)			
DT	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)			

Query Match	Similarity	Score	DB %	Length
Best Local	46%	Conservative	7.7%	31.1%
Matches	46%	Conservative	21%	Mismatches 65; Indels 11; Gaps 9
Db	49	yvhsknstactckhkytvsdgsppgdvrccekyttsaagylrgcjscktrke	108	
Qy	31	yDENSTSHOLCKCPPTLYLKQHCITAK-KMTVCACPDPHYTDSMHSDECLCSPVCKE	89	
Db	109	msgveispqadkdvcegcenkqfyrlsesthgvcdspcfng-tytlipketqntn	167	
Qy	90	LQYVK-QECNRHNHRCVCKG--RIL-DIEF-CLKHSCSPGGVGOAOTPERNTVCK	143	
Db	168	-chagflfresceyposhknec	191	
Qy	144	RCPDGFFSNETSCKA-P-CRKATNC	166	
RESULT	11	STANDARD:	PRT:	461 AA.
ID	TNR1_RAT			
AC	P22934:			
DT	01-MAR-1991 (REL. 19, LAST SEQUENCE UPDATE)			
DT	01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)			
DT	01-NOV-1993 (REL. 32, LAST ANNOTATION UPDATE)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).			
GN	TNFR1 OR TNFR-1.			
OS	RATU5 NORVEGICUS (RAT).			
OS	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
OC	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE; 91090841.			
RX	HIMMLER A., MAURER-FOGY I., KROENKE M., SCHURICH P., PRIZENMAIER K.,			
RA	HIMMLER A., OLSSON I., HAUPTMANN R., STRATOWA C., ADOLF G.R.;			
RA	LANTZ M., OLSSON I., 9:705-715(1990).			
RL	DNA CELL BIOL. 9:705-715(1990).			
CC	-1- FUNCTION: RECEPTOR FOR TNF-ALPHA.			
CC	-1- CELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	EMBL: M63122; G207362; .			
DR	PIR; B36555; B36555.			
DR	PIR; B36555; B36555.			
DR	HSSP; P19438; 11NR.			
DR	PROSITE; P850652; TNFR-NGFR.			
DR	PROSITE; P850017; DEATH DOMAIN.			
KW	RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGML.			
FT	SIGML	1	21	
FT	CHAIN	22	455	
FT	DOMAIN	22	211	
FT	TRANSMEM	212	234	
FT	DOMAIN	235	461	
FT	DOMAIN	43	196	
FT	REPEAT	43	82	
FT	REPEAT	83	125	
FT	REPEAT	126	166	
FT	REPEAT	167	196	
FT	DOMAIN	363	448	
FT	DOMAIN	44	58	
FT	DISULFID	59	72	
FT	DISULFID	62	81	
FT	DISULFID	84	99	
FT	DISULFID	102	117	

```

FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 185 195 BY SIMILARITY.
FT CARBOHYD 54 54 POTENTIAL.
FT CARBOHYD 151 151 POTENTIAL.
FT CARBOHYD 201 201 POTENTIAL.
SQ SEQUENCE 461 AA; 50969 MM; 82F68B08 CRC32;

Query Match
Best Local Similarity 33.8%; Score 220; DB 9; Length 461;
Matches 49; Conservative 22; Mismatches 63; Indels 11; Gaps 10;

Db
49 yabphnslctckhkytlvsdcpdpqgevcckgftasqnhvrgclskctcke 108
31 YDETSHQLLCDKCPGTYLKQCHCTAK-WKTVGAPCPDHYYTDSWHTSDCLYCSPVCKE 89
109 mfgvelspckadmtvcgckngfyrlsethfgcvdcspcfng-cvllpckekqntvcn 167
90 L-QYVKQECNRRHNRVCECK--E-GRTL-EIEF-CLKHRSCTPGFGVYAGTPEBNTVCK 143
168 -chagfflsgnecpshckngdec 191
144 RCPDGF-S-NEISSKAPCRKHTNC 166

RESULT 12
ID NGFR-CHICK STANDARD; PRT; 416 AA.
AC P18519;
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LNGFR).
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 90166579.
RA LARGE T.H., WESEKAMP G., HELDER J.C., RADEKE M.J., MISKO T.P.,
RA SHOOTER E.N., REICHARDT L.F.;
RA NEURON 2:1123-1134(1989).
[2]
[3]
[4]
[5]
[6]
[7]
[8]
[9]
[10]
[11]
[12]
[13]
[14]
[15]
[16]
[17]
[18]
[19]
[20]
[21]
[22]
[23]
[24]
[25]
[26]
[27]
[28]
[29]
[30]
[31]
[32]
[33]
[34]
[35]
[36]
[37]
[38]
[39]
[40]
[41]
[42]
[43]
[44]
[45]
[46]
[47]
[48]
[49]
[50]
[51]
[52]
[53]
[54]
[55]
[56]
[57]
[58]
[59]
[60]
[61]
[62]
[63]
[64]
[65]
[66]
[67]
[68]
[69]
[70]
[71]
[72]
[73]
[74]
[75]
[76]
[77]
[78]
[79]
[80]
[81]
[82]
[83]
[84]
[85]
[86]
[87]
[88]
[89]
[90]
[91]
[92]
[93]
[94]
[95]
[96]
[97]
[98]
[99]
[100]
[101]
[102]
[103]
[104]
[105]
[106]
[107]
[108]
[109]
[110]
[111]
[112]
[113]
[114]
[115]
[116]
[117]
[118]
[119]
[120]
[121]
[122]
[123]
[124]
[125]
[126]
[127]
[128]
[129]
[130]
[131]
[132]
[133]
[134]
[135]
[136]
[137]
[138]
[139]
[140]
[141]
[142]
[143]
[144]
[145]
[146]
[147]
[148]
[149]
[150]
[151]
[152]
[153]
[154]
[155]
[156]
[157]
[158]
[159]
[160]
[161]
[162]
[163]
[164]
[165]
[166]
[167]
[168]
[169]
[170]
[171]
[172]
[173]
[174]
[175]
[176]
[177]
[178]
[179]
[180]
[181]
[182]
[183]
[184]
[185]
[186]
[187]
[188]
[189]
[190]
[191]
[192]
[193]
[194]
[195]
[196]
[197]
[198]
[199]
[200]
[201]
[202]
[203]
[204]
[205]
[206]
[207]
[208]
[209]
[210]
[211]
[212]
[213]
[214]
[215]
[216]
[217]
[218]
[219]
[220]
[221]
[222]
[223]
[224]
[225]
[226]
[227]
[228]
[229]
[230]
[231]
[232]
[233]
[234]
[235]
[236]
[237]
[238]
[239]
[240]
[241]
[242]
[243]
[244]
[245]
[246]
[247]
[248]
[249]
[250]
[251]
[252]
[253]
[254]
[255]
[256]
[257]
[258]
[259]
[260]
[261]
[262]
[263]
[264]
[265]
[266]
[267]
[268]
[269]
[270]
[271]
[272]
[273]
[274]
[275]
[276]
[277]
[278]
[279]
[280]
[281]
[282]
[283]
[284]
[285]
[286]
[287]
[288]
[289]
[290]
[291]
[292]
[293]
[294]
[295]
[296]
[297]
[298]
[299]
[300]
[301]
[302]
[303]
[304]
[305]
[306]
[307]
[308]
[309]
[310]
[311]
[312]
[313]
[314]
[315]
[316]
[317]
[318]
[319]
[320]
[321]
[322]
[323]
[324]
[325]
[326]
[327]
[328]
[329]
[330]
[331]
[332]
[333]
[334]
[335]
[336]
[337]
[338]
[339]
[340]
[341]
[342]
[343]
[344]
[345]
[346]
[347]
[348]
[349]
[350]
[351]
[352]
[353]
[354]
[355]
[356]
[357]
[358]
[359]
[360]
[361]
[362]
[363]
[364]
[365]
[366]
[367]
[368]
[369]
[370]
[371]
[372]
[373]
[374]
[375]
[376]
[377]
[378]
[379]
[380]
[381]
[382]
[383]
[384]
[385]
[386]
[387]
[388]
[389]
[390]
[391]
[392]
[393]
[394]
[395]
[396]
[397]
[398]
[399]
[400]
[401]
[402]
[403]
[404]
[405]
[406]
[407]
[408]
[409]
[410]
[411]
[412]
[413]
[414]
[415]
[416]
[417]
[418]
[419]
[420]
[421]
[422]
[423]
[424]
[425]
[426]
[427]
[428]
[429]
[430]
[431]
[432]
[433]
[434]
[435]
[436]
[437]
[438]
[439]
[440]
[441]
[442]
[443]
[444]
[445]
[446]
[447]
[448]
[449]
[450]
[451]
[452]
[453]
[454]
[455]
[456]
[457]
[458]
[459]
[460]
[461]
[462]
[463]
[464]
[465]
[466]
[467]
[468]
[469]
[470]
[471]
[472]
[473]
[474]
[475]
[476]
[477]
[478]
[479]
[480]
[481]
[482]
[483]
[484]
[485]
[486]
[487]
[488]
[489]
[490]
[491]
[492]
[493]
[494]
[495]
[496]
[497]
[498]
[499]
[500]
[501]
[502]
[503]
[504]
[505]
[506]
[507]
[508]
[509]
[510]
[511]
[512]
[513]
[514]
[515]
[516]
[517]
[518]
[519]
[520]
[521]
[522]
[523]
[524]
[525]
[526]
[527]
[528]
[529]
[530]
[531]
[532]
[533]
[534]
[535]
[536]
[537]
[538]
[539]
[540]
[541]
[542]
[543]
[544]
[545]
[546]
[547]
[548]
[549]
[550]
[551]
[552]
[553]
[554]
[555]
[556]
[557]
[558]
[559]
[560]
[561]
[562]
[563]
[564]
[565]
[566]
[567]
[568]
[569]
[570]
[571]
[572]
[573]
[574]
[575]
[576]
[577]
[578]
[579]
[580]
[581]
[582]
[583]
[584]
[585]
[586]
[587]
[588]
[589]
[590]
[591]
[592]
[593]
[594]
[595]
[596]
[597]
[598]
[599]
[600]
[601]
[602]
[603]
[604]
[605]
[606]
[607]
[608]
[609]
[610]
[611]
[612]
[613]
[614]
[615]
[616]
[617]
[618]
[619]
[620]
[621]
[622]
[623]
[624]
[625]
[626]
[627]
[628]
[629]
[630]
[631]
[632]
[633]
[634]
[635]
[636]
[637]
[638]
[639]
[640]
[641]
[642]
[643]
[644]
[645]
[646]
[647]
[648]
[649]
[650]
[651]
[652]
[653]
[654]
[655]
[656]
[657]
[658]
[659]
[660]
[661]
[662]
[663]
[664]
[665]
[666]
[667]
[668]
[669]
[670]
[671]
[672]
[673]
[674]
[675]
[676]
[677]
[678]
[679]
[680]
[681]
[682]
[683]
[684]
[685]
[686]
[687]
[688]
[689]
[690]
[691]
[692]
[693]
[694]
[695]
[696]
[697]
[698]
[699]
[700]
[701]
[702]
[703]
[704]
[705]
[706]
[707]
[708]
[709]
[710]
[711]
[712]
[713]
[714]
[715]
[716]
[717]
[718]
[719]
[720]
[721]
[722]
[723]
[724]
[725]
[726]
[727]
[728]
[729]
[730]
[731]
[732]
[733]
[734]
[735]
[736]
[737]
[738]
[739]
[740]
[741]
[742]
[743]
[744]
[745]
[746]
[747]
[748]
[749]
[750]
[751]
[752]
[753]
[754]
[755]
[756]
[757]
[758]
[759]
[760]
[761]
[762]
[763]
[764]
[765]
[766]
[767]
[768]
[769]
[770]
[771]
[772]
[773]
[774]
[775]
[776]
[777]
[778]
[779]
[780]
[781]
[782]
[783]
[784]
[785]
[786]
[787]
[788]
[789]
[790]
[791]
[792]
[793]
[794]
[795]
[796]
[797]
[798]
[799]
[800]
[801]
[802]
[803]
[804]
[805]
[806]
[807]
[808]
[809]
[810]
[811]
[812]
[813]
[814]
[815]
[816]
[817]
[818]
[819]
[820]
[821]
[822]
[823]
[824]
[825]
[826]
[827]
[828]
[829]
[830]
[831]
[832]
[833]
[834]
[835]
[836]
[837]
[838]
[839]
[840]
[841]
[842]
[843]
[844]
[845]
[846]
[847]
[848]
[849]
[850]
[851]
[852]
[853]
[854]
[855]
[856]
[857]
[858]
[859]
[860]
[861]
[862]
[863]
[864]
[865]
[866]
[867]
[868]
[869]
[870]
[871]
[872]
[873]
[874]
[875]
[876]
[877]
[878]
[879]
[880]
[881]
[882]
[883]
[884]
[885]
[886]
[887]
[888]
[889]
[890]
[891]
[892]
[893]
[894]
[895]
[896]
[897]
[898]
[899]
[900]
[901]
[902]
[903]
[904]
[905]
[906]
[907]
[908]
[909]
[910]
[911]
[912]
[913]
[914]
[915]
[916]
[917]
[918]
[919]
[920]
[921]
[922]
[923]
[924]
[925]
[926]
[927]
[928]
[929]
[930]
[931]
[932]
[933]
[934]
[935]
[936]
[937]
[938]
[939]
[940]
[941]
[942]
[943]
[944]
[945]
[946]
[947]
[948]
[949]
[950]
[951]
[952]
[953]
[954]
[955]
[956]
[957]
[958]
[959]
[960]
[961]
[962]
[963]
[964]
[965]
[966]
[967]
[968]
[969]
[970]
[971]
[972]
[973]
[974]
[975]
[976]
[977]
[978]
[979]
[980]
[981]
[982]
[983]
[984]
[985]
[986]
[987]
[988]
[989]
[990]
[991]
[992]
[993]
[994]
[995]
[996]
[997]
[998]
[999]
[1000]

```

```

FT REPEAT 101 140 TNFR-CYS 3.
FT REPEAT 141 181 TNFR-CYS 4.
FT DOMAIN 188 226 SER/THR-RICH.
FT DOMAIN 333 410 DEATH DOMAIN.
FT DISULFID 24 35 BY SIMILARITY.
FT DISULFID 36 49 BY SIMILARITY.
FT DISULFID 39 56 BY SIMILARITY.
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 78 91 BY SIMILARITY.
FT DISULFID 81 99 BY SIMILARITY.
FT DISULFID 101 114 BY SIMILARITY.
FT DISULFID 117 130 BY SIMILARITY.
FT DISULFID 120 138 BY SIMILARITY.
FT DISULFID 141 156 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 162 180 BY SIMILARITY.
FT CARBOHYD 52 52 POTENTIAL.
FT CARBOHYD 36 36 C -> Y (IN REF. 2).
FT CONFLICT 173 173 T -> K (IN REF. 2).
FT CONFLICT 276 276 N -> S (IN REF. 2).
FT CONFLICT 396 396 K -> R (IN REF. 2).
SQ SEQUENCE 416 AA; 44654 MM; 4D3F086A CRC32;

Query Match
Best Local Similarity 30.4%; Score 215; DB 6; Length 416;
Matches 45; Conservative 27; Mismatches 70; Indels 6; Gaps 6;

Db
36 ckaenlgevgvpcgyn-dtvepcldsvtdvatsatepckpctg-cvylhmsapcve 93
41 CDKCPGTYLKQCHCTAKWKTVGAPCPDH-YTDSWHTSDCLYCSPVCKELQVQKCHNR 99
94 sdavrcrcayyfgdelssckscsicevgfmlfpcrsgdtveceopcgtsdeanfv 153
100 THRVCECKEGRTL-EIE-FCLKHRSCTPGFGVYAGTPEBNTVCKRCRCPDGFSSNETSSK 157
154 dpcplcticeenwmyke-ctatsdaec 180
158 APCKRHTNCSVFGLLTQKGNATHDNIC 185

RESULT 13
ID NGFR-HUMAN STANDARD; PRT; 427 AA.
AC P08138;
DT 01-AUG-1988 (REL. 08, CREATED)
DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
DE (GP80-LNGFR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 87051725.
RA JOHNSON D., LANAHAN A., BUCK C.R., SEHGAL A., MORGAN C., MERCER E.,
RA BOTWELL M., CHAO M.;
RA CELL 47:545-554(1986).
[2]
[3]
[4]
[5]
[6]
[7]
[8]
[9]
[10]
[11]
[12]
[13]
[14]
[15]
[16]
[17]
[18]
[19]
[20]
[21]
[22]
[23]
[24]
[25]
[26]
[27]
[28]
[29]
[30]
[31]
[32]
[33]
[34]
[35]
[36]
[37]
[38]
[39]
[40]
[41]
[42]
[43]
[44]
[45]
[46]
[47]
[48]
[49]
[50]
[51]
[52]
[53]
[54]
[55]
[56]
[57]
[58]
[59]
[60]
[61]
[62]
[63]
[64]
[65]
[66]
[67]
[68]
[69]
[70]
[71]
[72]
[73]
[74]
[75]
[76]
[77]
[78]
[79]
[80]
[81]
[82]
[83]
[84]
[85]
[86]
[87]
[88]
[89]
[90]
[91]
[92]
[93]
[94]
[95]
[96]
[97]
[98]
[99]
[100]
[101]
[102]
[103]
[104]
[105]
[106]
[107]
[108]
[109]
[110]
[111]
[112]
[113]
[114]
[115]
[116]
[117]
[118]
[119]
[120]
[121]
[122]
[123]
[124]
[125]
[126]
[127]
[128]
[129]
[130]
[131]
[132]
[133]
[134]
[135]
[136]
[137]
[138]
[139]
[140]
[141]
[142]
[143]
[144]
[145]
[146]
[147]
[148]
[149]
[150]
[151]
[152]
[153]
[154]
[155]
[156]
[157]
[158]
[159]
[160]
[161]
[162]
[163]
[164]
[165]
[166]
[167]
[168]
[169]
[170]
[171]
[172]
[173]
[174]
[175]
[176]
[177]
[178]
[179]
[180]
[181]
[182]
[183]
[184]
[185]
[186]
[187]
[188]
[189]
[190]
[191]
[192]
[193]
[194]
[195]
[196]
[197]
[198]
[199]
[200]
[201]
[202]
[203]
[204]
[205]
[206]
[207]
[208]
[209]
[210]
[211]
[212]
[213]
[214]
[215]
[216]
[217]
[218]
[219]
[220]
[221]
[222]
[223]
[224]
[225]
[226]
[227]
[228]
[229]
[230]
[231]
[232]
[233]
[234]
[235]
[236]
[237]
[238]
[239]
[240]
[241]
[242]
[243]
[244]
[245]
[246]
[247]
[248]
[249]
[250]
[251]
[252]
[253]
[254]
[255]
[256]
[257]
[258]
[259]
[260]
[261]
[262]
[263]
[264]
[265]
[266]
[267]
[268]
[269]
[270]
[271]
[272]
[273]
[274]
[275]
[276]
[277]
[278]
[279]
[280]
[281]
[282]
[283]
[284]
[285]
[286]
[287]
[288]
[289]
[290]
[291]
[292]
[293]
[294]
[295]
[296]
[297]
[298]
[299]
[300]
[301]
[302]
[303]
[304]
[305]
[306]
[307]
[308]
[309]
[310]
[311]
[312]
[313]
[314]
[315]
[316]
[317]
[318]
[319]
[320]
[321]
[322]
[323]
[324]
[325]
[326]
[327]
[328]
[329]
[330]
[331]
[332]
[333]
[334]
[335]
[336]
[337]
[338]
[339]
[340]
[341]
[342]
[343]
[344]
[345]
[346]
[347]
[348]
[349]
[350]
[351]
[352]
[353]
[354]
[355]
[356]
[357]
[358]
[359]
[360]
[361]
[362]
[363]
[364]
[365]
[366]
[367]
[368]
[369]
[370]
[371]
[372]
[373]
[374]
[375]
[376]
[377]
[378]
[379]
[380]
[381]
[382]
[383]
[384]
[385]
[386]
[387]
[388]
[389]
[390]
[391]
[392]
[393]
[394]
[395]
[396]
[397]
[398]
[399]
[400]
[401]
[402]
[403]
[404]
[405]
[406]
[407]
[408]
[409]
[410]
[411]
[412]
[413]
[414]
[415]
[416]
[417]
[418]
[419]
[420]
[421]
[422]
[423]
[424]
[425]
[426]
[427]
[428]
[429]
[430]
[431]
[432]
[433]
[434]
[435]
[436]
[437]
[438]
[439]
[440]
[441]
[442]
[443]
[444]
[445]
[446]
[447]
[448]
[449]
[450]
[451]
[452]
[453]
[454]
[455]
[456]
[457]
[458]
[459]
[460]
[461]
[462]
[463]
[464]
[465]
[466]
[467]
[468]
[469]
[470]
[471]
[472]
[473]
[474]
[475]
[476]
[477]
[478]
[479]
[480]
[481]
[482]
[483]
[484]
[485]
[486]
[487]
[488]
[489]
[490]
[491]
[492]
[493]
[494]
[495]
[496]
[497]
[498]
[499]
[500]
[501]
[502]
[503]
[504]
[505]
[506]
[507]
[508]
[509]
[510]
[511]
[512]
[513]
[514]
[515]
[516]
[517]
[518]
[519]
[520]
[521]
[522]
[523]
[524]
[525]
[526]
[527]
[528]
[529]
[530]
[531]
[532]
[533]
[534]
[535]
[536]
[537]
[538]
[539]
[540]
[541]
[542]
[543]
[544]
[545]
[546]
[547]
[548]
[549]
[550]
[551]
[552]
[553]
[554]
[555]
[556]
[557]
[558]
[559]
[560]
[561]
[562]
[563]
[564]
[565]
[566]
[567]
[568]
[569]
[570]
[571]
[572]
[573]
[574]
[575]
[576]
[577]
[578]
[579]
[580]
[581]
[582]
[583]
[584]
[585]
[586]
[587]
[588]
[589]
[590]
[591]
[592]
[593]
[594]
[595]
[596]
[597]
[598]
[599]
[600]
[601]
[602]
[603]
[604]
[605]
[606]
[607]
[608]
[609]
[610]
[611]
[612]
[613]
[614]
[615]
[616]
[617]
[618]
[619]
[620]
[621]
[622]
[623]
[624]
[625]
[626]
[627]
[628]
[629]
[630]
[631]
[632]
[633]
[634]
[635]
[636]
[637]
[638]
[639]
[640]
[641]
[642]
[643]
[644]
[645]
[646]
[647]
[648]
[649]
[650]
[651]
[652]
[653]
[654]
[655]
[656]
[657]
[658]
[659]
[660]
[661]
[662]
[663]
[664]
[665]
[666]
[667]
[668]
[669]
[670]
[671]
[672]
[673]
[674]
[675]
[676]
[677]
[678]
[679]
[680]
[681]
[682]
[683]
[684]
[685]
[686]
[687]
[688]
[689]
[690]
[691]
[692]
[693]
[694]
[695]
[696]
[697]
[698]
[699]
[700]
[701]
[702]
[703]
[704]
[705]
[706]
[707]
[708]
[709]
[710]
[711]
[712]
[713]
[714]
[715]
[716]
[717]
[718]
[719]
[720]
[721]
[722]
[723]
[724]
[725]
[726]
[727]
[728]
[729]
[730]
[731]
[732]
[733]
[734]
[735]
[736]
[737]
[738]
[739]
[740]
[741]
[742]
[743]
[744]
[745]
[746]
[747]
[748]
[749]
[750]
[751]
[752]
[753]
[754]
[755]
[756]
[757]
[758]
[759]
[760]
[761]
[762]
[763]
[764]
[765]
[766]
[767]
[768]
[769]
[770]
[771]
[772]
[773]
```

FT SIGNAL 1 28
 FT CHAIN 29 427
 FT DOMAIN 29 250
 FT TRANSMEM 251 272
 FT DOMAIN 273 427
 FT DOMAIN 31 189
 FT REPEAT 31 65
 FT REPEAT 66 107
 FT REPEAT 108 147
 FT REPEAT 148 189
 FT DOMAIN 344 421
 FT DISULFID 32 43
 FT DISULFID 44 57
 FT DISULFID 47 64
 FT DISULFID 67 83
 FT DISULFID 86 99
 FT DISULFID 89 107
 FT DISULFID 109 122
 FT DISULFID 125 138
 FT DISULFID 128 146
 FT DISULFID 149 164
 FT DISULFID 167 180
 FT DISULFID 170 188
 FT DISULFID 197 248
 FT DOMAIN 197 248
 FT CARBOHYD 60 60
 FT SEQUENCE 427 AA; 45183 MW; EE2924BD CRC32;

Query Match 7.48; Score 213; DB 6; Length 427;
 Best Local Similarity 34.9%; Pred. No. 1.81e-21;
 Matches 45; Conservative 19; Mismatches 60; Indels 5; Gaps 5;

Db 44 ckaenlgeyagvqpgan-qtvepcldsvtfsdvsatepckpcte-cvlgmsapve 101
 Oy 41 CDKCPGGTYLKQHCIAKKTVCAPCPDH-YTDSMHTSDCLCSPVCKELQVYKQECNR 99
 Db 102 addavrcaygygdeetgicacvceagsglyfscqdkqntvcecpdqtysdeanhv 161
 Oy 100 THNRVCECKEGRYLEIE-FCLKHRSCPPGFGVQAGTPERNIVCKRCPDGFNSSTSSK 157
 Db 162 dpcldpctvc 170
 Oy 158 APCRKHNC 166

RESULT 14 STANDARD: PRT: 425 AA.
 ID NGFR RAT
 AC P07174;
 01-APR-1988 (REL. 07, CREATED)
 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-LINGFR).
 CN NGFR.
 OS RATTUS NORVEGICUS (RAT).
 OS EURARCTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 CC [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 87115859.
 RA RADEKE M.J., MISKO T.P., HSU C., HERZENBERG L.A., SHOOTER E.M.;
 RL NATURE 325:593-597(1987).
 RN [2]
 RP SEQUENCE OF 1-22 FROM N.A.
 RC TISSUE-LIVER.
 RX MEDLINE: 93077038.
 RA METSIS M., TIMOSK T., ALLIKMETS R., SAARMA M., PERSSON H.;
 RL GENE 121:247-254(1992).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 CC -1- NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 CC -1- BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: X05137; G56736;
 DR EMBL: X61269; -; NOT_ANNOTATED_CDS.
 DR PIR: A26431; A26431.
 DR HSSP: P19438; 1TNR.
 DR PROSITE: P500652; TNFR_NGFR.
 DR PROSITE: P500017; DEATH_DOMAIN.
 DR RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;
 KW PHOSPHORYLATION; SIGNAL.
 FT SIGNAL 1 29
 FT CHAIN 30 425
 FT DOMAIN 30 251
 FT TRANSMEM 252 273
 FT DOMAIN 274 425
 FT DOMAIN 32 190
 FT REPEAT 32 66
 FT REPEAT 67 108
 FT REPEAT 109 148
 FT REPEAT 149 190
 FT DOMAIN 198 249
 FT DISULFID 33 44
 FT DISULFID 45 58
 FT DISULFID 48 65
 FT DISULFID 68 84
 FT DISULFID 87 100
 FT DISULFID 90 108
 FT DISULFID 110 123
 FT DISULFID 126 139
 FT DISULFID 129 147
 FT DISULFID 150 165
 FT DISULFID 168 181
 FT DISULFID 171 189
 FT DISULFID 61 61
 FT CARBOHYD 71 71
 FT SEQUENCE 425 AA; 45432 MW; 7D78F258 CRC32;

Query Match 7.28; Score 207; DB 6; Length 425;
 Best Local Similarity 33.3%; Pred. No. 2.85e-20;
 Matches 43; Conservative 21; Mismatches 60; Indels 5; Gaps 4;

Db 45 ckaenlgeyagvqpgan-qtvepcldsvtfsdvsatepckpcte-clvgmsapve 102
 Oy 41 CDKCPGGTYLKQHCIAKKTVCAPCPDH-YTDSMHTSDCLCSPVCKELQVYKQECNR 99
 Db 103 addavrcaygygdeetgicacvceagsglyfscqdkqntvcecpdqtysdeanhv 162
 Oy 100 THNRVCECKEGRYLEIE-FCLKHRSCPPGFGVQAGTPERNIVCKRCPDGFNSSTSSK 157
 Db 163 dpcldpctvc 171
 Oy 158 APCRKHNC 166

RESULT 15 STANDARD: PRT: 323 AA.
 ID FASA BOVIN
 AC P51867;
 01-OCT-1996 (REL. 34, CREATED)
 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
 DE (APO-1 ANTIGEN) (CD95).
 CN APT1 OR FAS.
 OS BOS TAURUS (BOVINE).
 OS EURARCTA: METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 CC [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 96226401.
 RA YOO J., STONE R.T., BEATTIE C.W.;
 RL DNA CELL BIOD. 15:227-234(1996).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. MEDIATES
 CC -1- CELL DEATH. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE

THIS PAGE BLANK (USPTO)